Lane	1	2	3	4	5	6	7	8
Biotinylation	+	+	+	+	+	+	+	+
791T/36	+	-	+	-	+	-	+	-
1143/B7	-	+	-	+	-	+	-	+
DTSSP	-	-	+	+	-	-	+	+
Solublisation	x	x	x	x	o	o	o	o

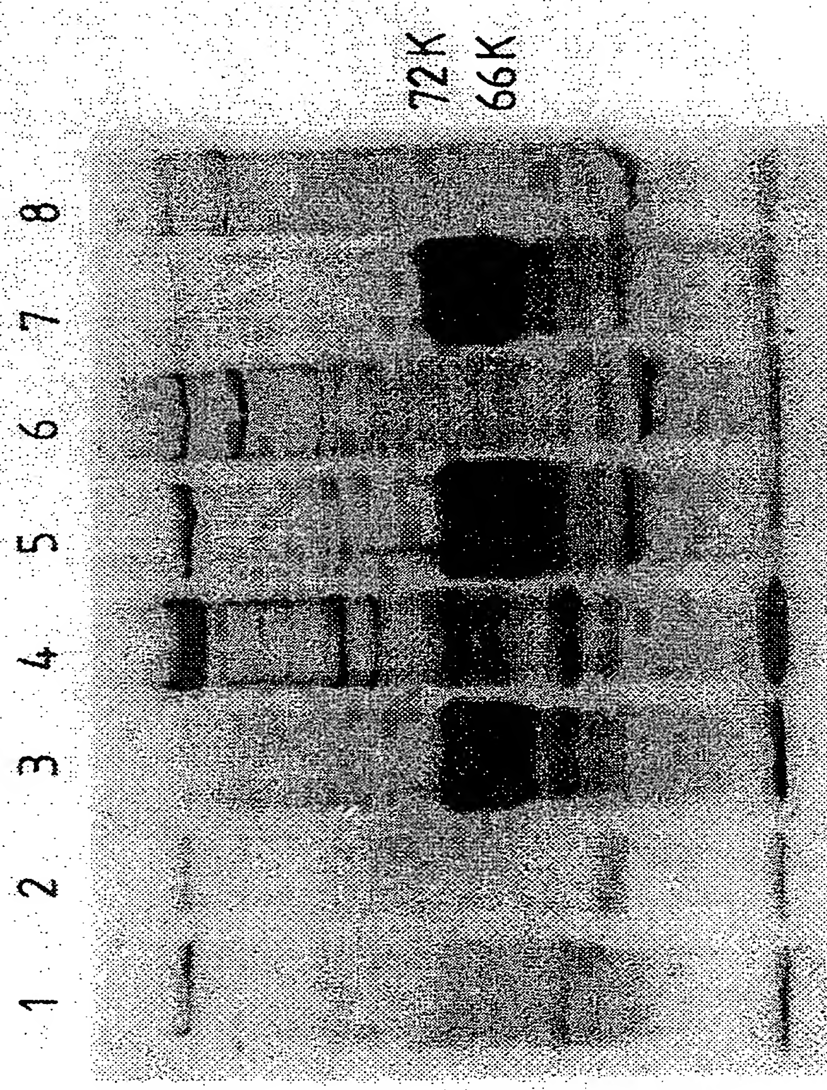

Fig. 1

Detergent						
Glucoside	+	-	-	-	-	-
NP-40	-	+	-	-	-	-
TX-100	-	-	+	+	+	+
Centrifugation						
13000 rpm	+	+	+	+	+	+
100, 000 g	+	+	+	-	+	+
blue-2	-	-	-	-	+	+

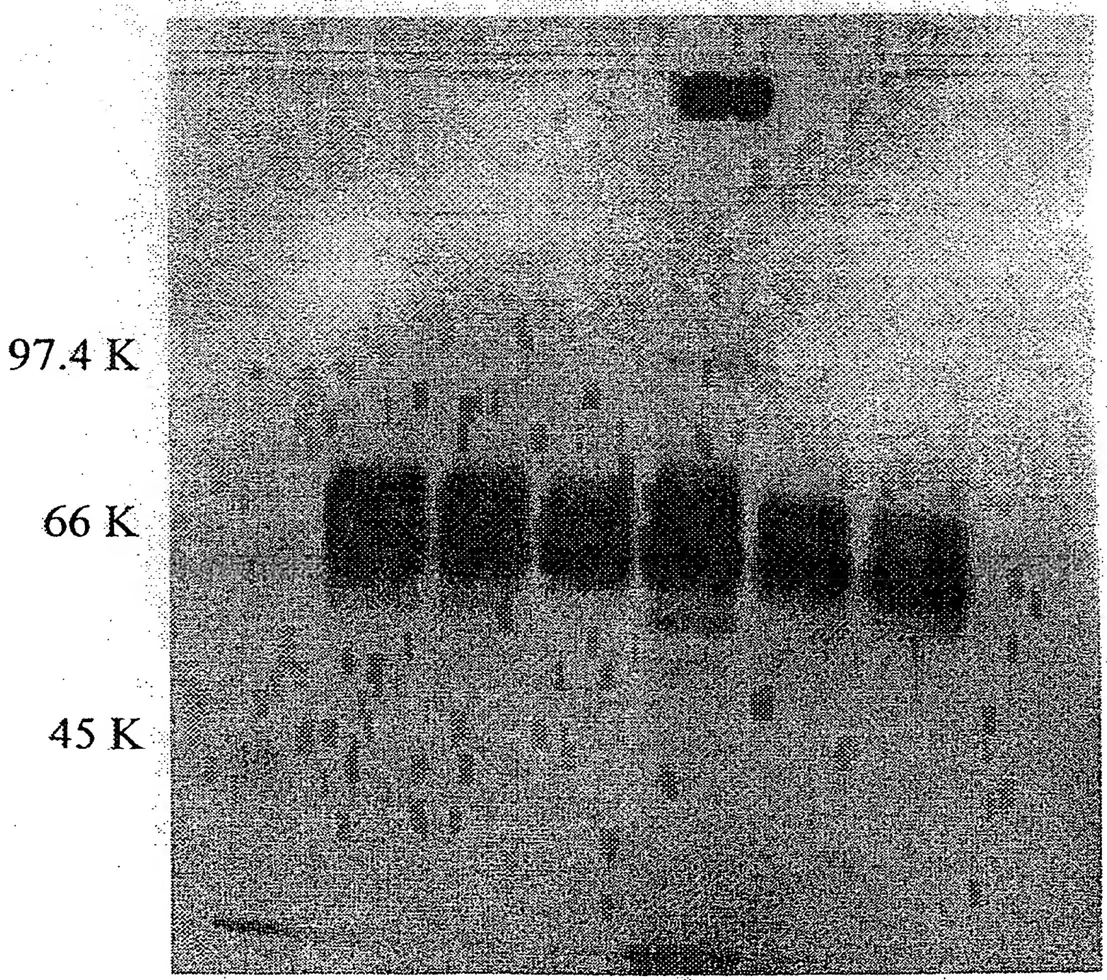

Fig. 2

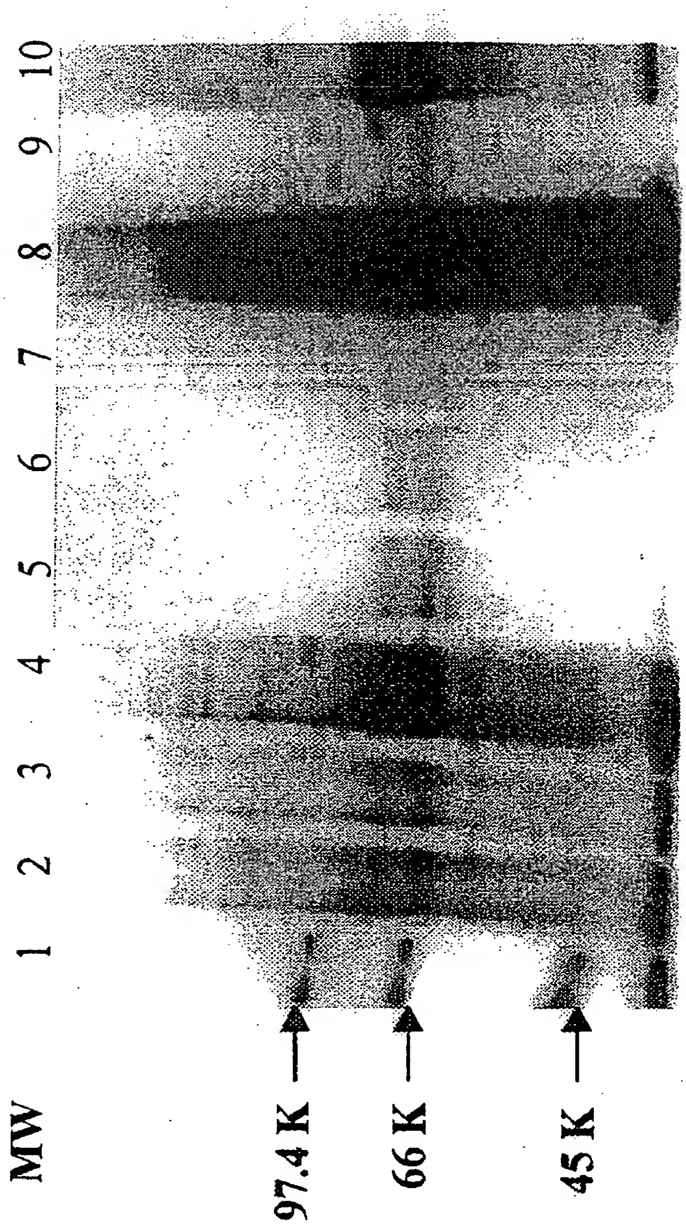

Fig. 3

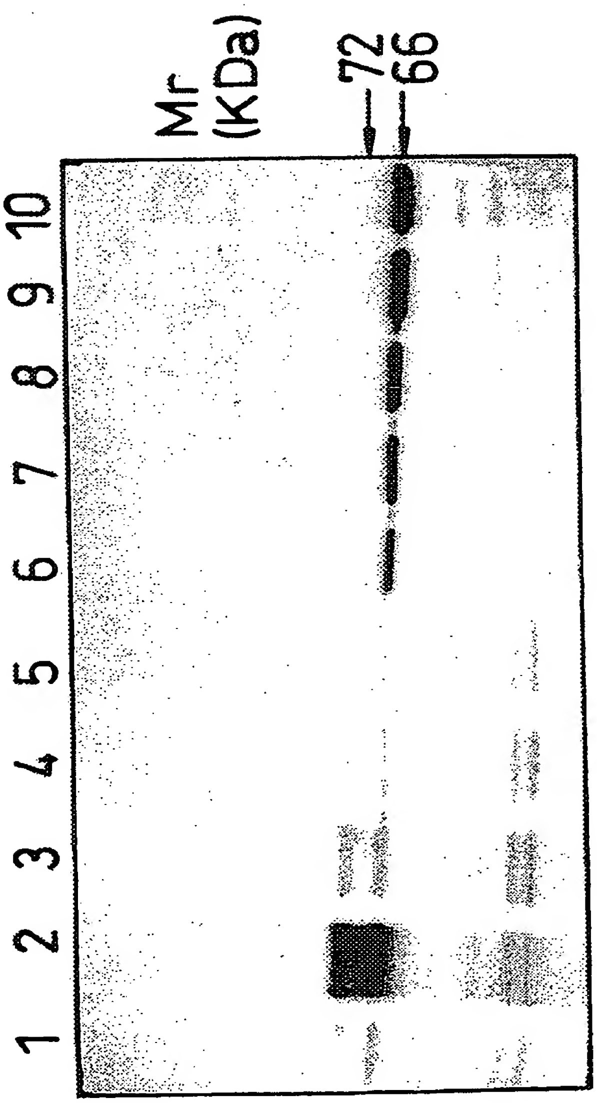

Fig. 4

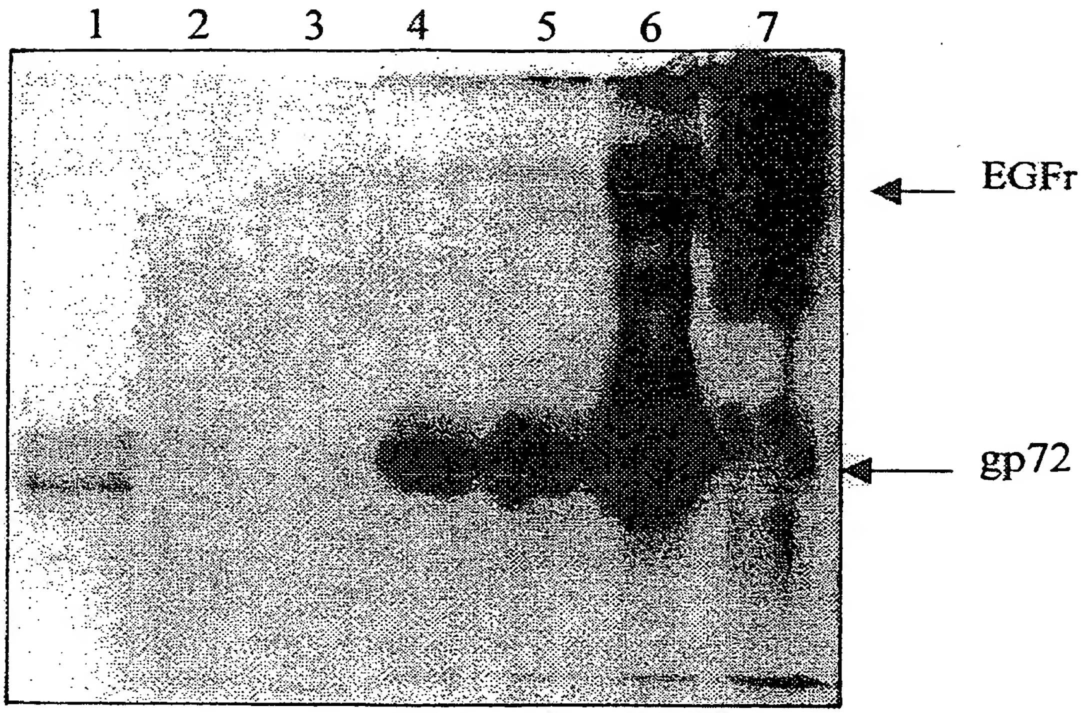

Fig. 5

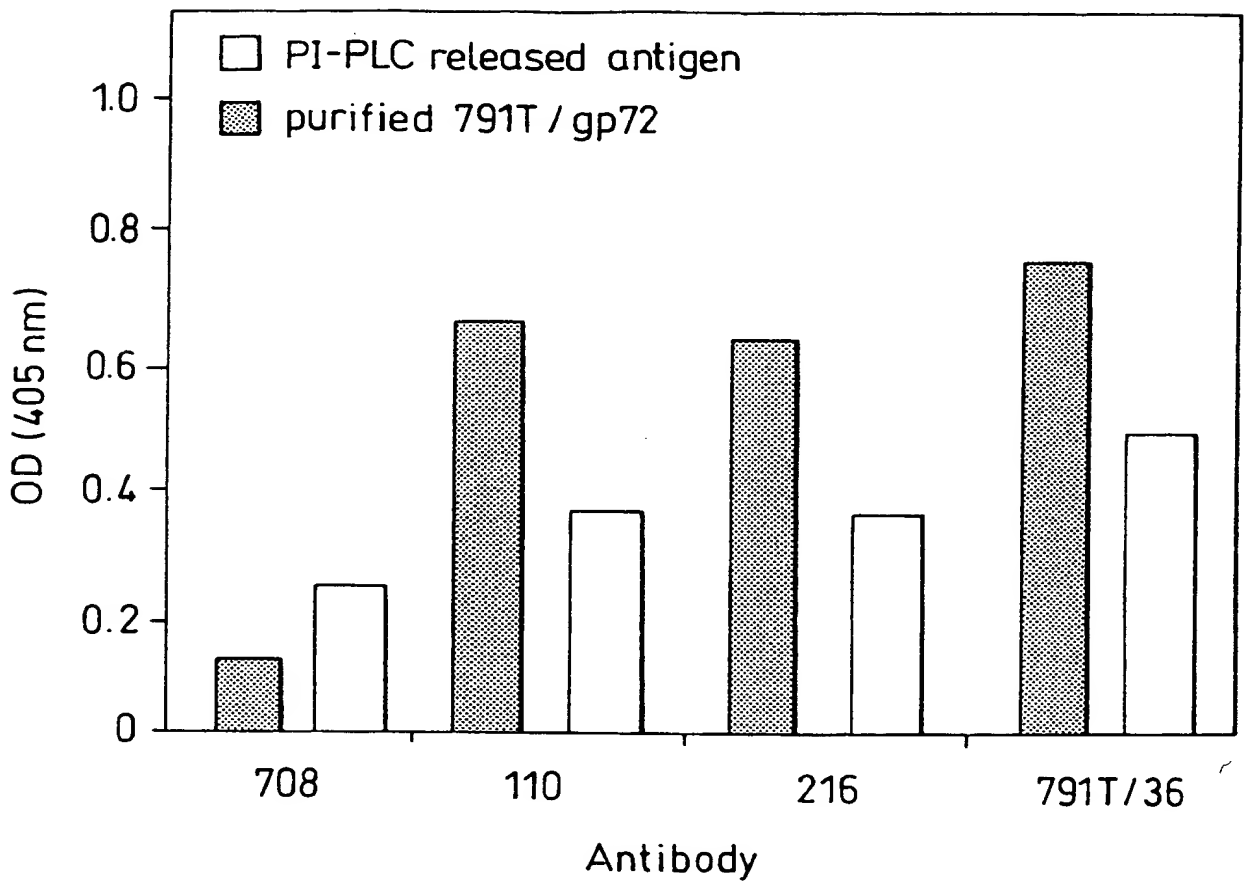
PI-PLC released antigen
purified 791T / gp72
1.0
0.8
0.6
0.4
0.2
0
OD (405 nm)
708
110
216
791T/36
Antibody

Fig. 6

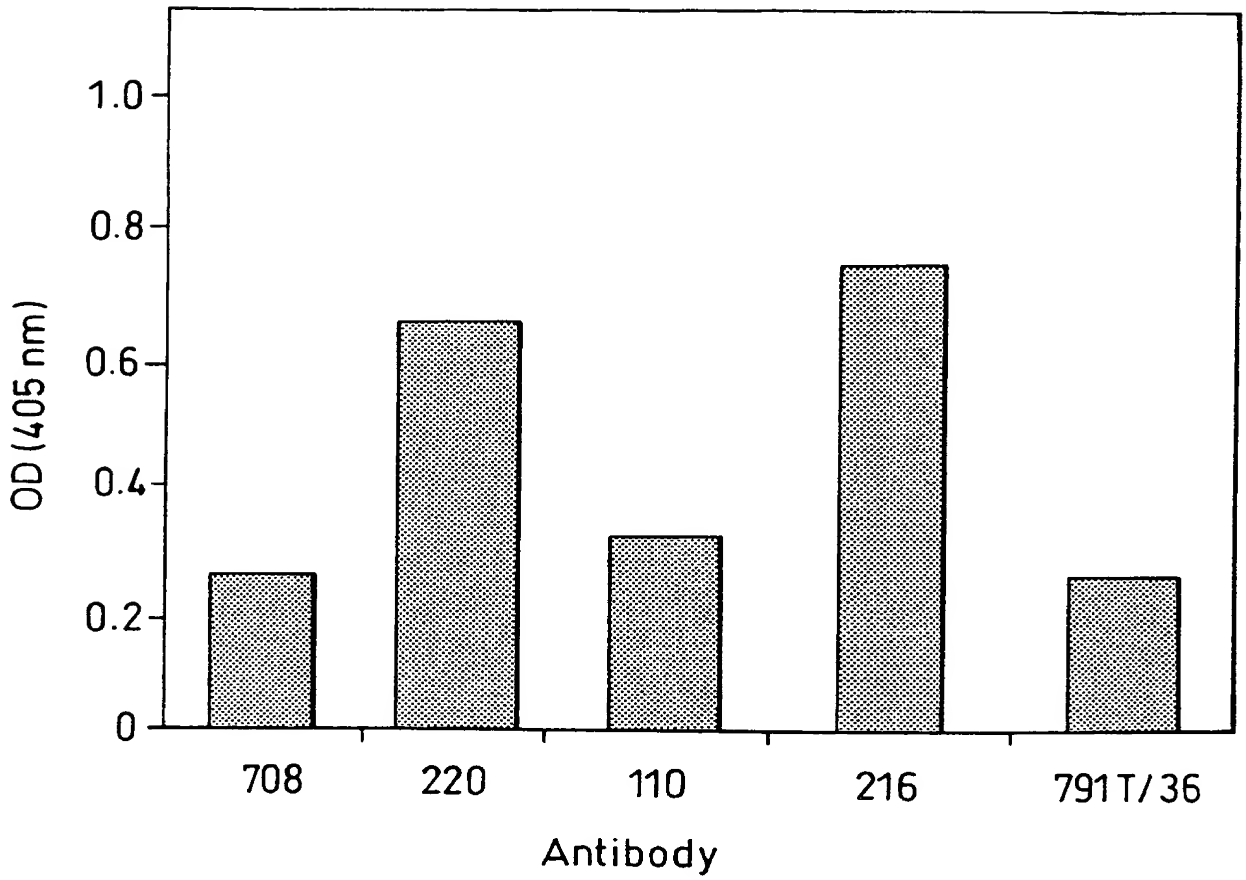

Fig. 7

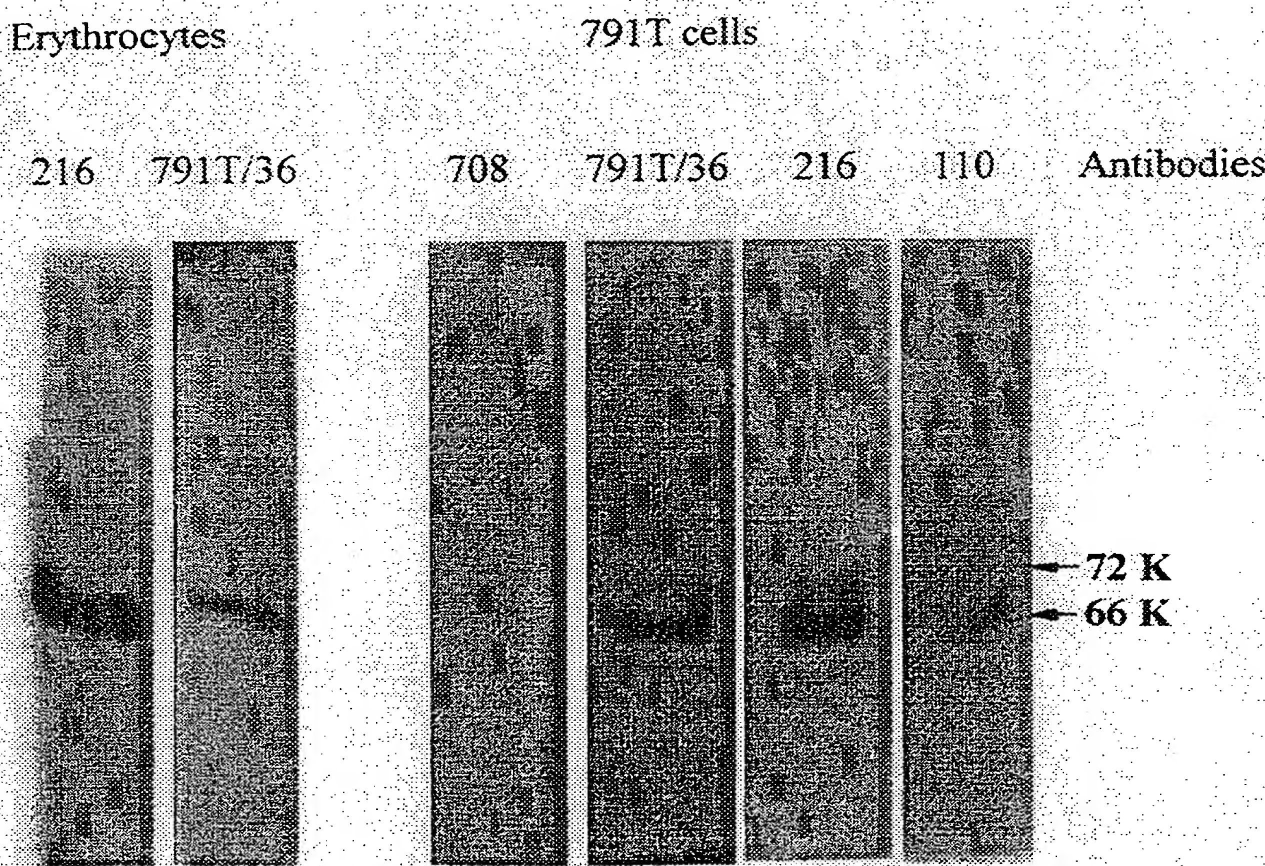
Erythrocytes
791T cells
216
791T/36
708
791T/36
216
110
Antibodies
72 K
66 K

Fig. 8

```
                         10        20        30        40        50
                          |         |         |         |         |
5/P5            ----------------------------------------------------------
C-DAF.seq       CCGCTGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCG
RC of B/C DAF   ----------------------------------------------------------

                 60        70        80        90       100       110
                  |         |         |         |         |         |
5/P5            ----------------------------------------------------------
C-DAF.seq       GCGCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAG
RC of B/C DAF   ----------------------------------------------------------

                   120       130       140       150       160       170
                    |         |         |                   |         |
5/P5            ----------------------------------------------------------
C-DAF.seq       CTGCCCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTG
RC of B/C DAF   ----------------------------------------------------------
```

Fig. 9 (part 1 of 11)

```
                   180       190       200       210       220       230
                     |         |         |         |         |         |
5/P5          ---------------------------------------------GTACAAGTTTTCC
C-DAF.seq     GCCTTCCCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCC
RC of B/C DAF ----------------------------------------------------------

                     240       250       260       270       280       290
                       |         |         |         |         |         |
5/P5          CGAGGATACTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAG
C-DAF.seq     CGAGGATACTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAG
RC of B/C DAF ----------------------------------------------------------

                       300       310       320       330       340
                         |         |         |         |         |
5/P5          AAGGACTCAGTGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCA
C-DAF.seq     AAGGACTCAGTGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCA
RC of B/C DAF ----------------------------------------------------------
```

Fig. 9 (part 2 of 11)

```
               350       360       370       380       390       400
                |         |         |         |         |         |
5/P5           ATCGTAGCTGCGAGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATAT
C-DAF.seq      ATCGTAGCTGCGAGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATAT
RC of B/C DAF  ----------------------------------------------------------

                   410       420       430       440       450       460
                    |         |         |         |         |         |
5/P5           CACTCAGAATTATTTTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTAC
C-DAF.seq      CACTCAGAATTATTTTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTAC
RC of B/C DAF  ----------------------------------------------------------

                       470       480       490       500       510       520
                        |         |         |         |         |         |
5/P5           AGAAGAGAACCTTCTCTATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCA
C-DAF.seq      AGAAGAGAACCTTCTCTATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCA
RC of B/C DAF  ----------------------------------------------------------

                           530       540       550       560       570       580
                            |         |         |         |         |         |
5/P5           CAGCAGTCGAATTTTGTAAAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGG
C-DAF.seq      CAGCAGTCGAATTTTGTAAAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGG
RC of B/C DAF  ----------------------------------------------------------
```

Fig. 9 (part 3 of 11)

```
                         590       600       610       620       630
                           |         |         |         |         |
5/P5            TCAGATTGATGTACCAGGTGGCATATTATTTGATGCAACCATCTCCTTCTCATGTAA
C-DAF.seq       TCAGATTGATGTACCAGGTGGCATATTATTTGGTGCAACCATCTCCTTCTCATGTAA
RC of B/C DAF   -----------------------TATTATTTGNTGCAACCATTTCCTTTTCATGTAA

                640       650       660       670       680       690
                  |         |         |         |         |         |
5/P5            CACAGGGGTACAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTC
C-DAF.seq       CACAGGG-TACAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTC
RC of B/C DAF   CACANGG-TACAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTC

                  700       710       720       730       740       750
                    |         |         |         |         |         |
5/P5            TGTCCAGTGGAGTGACCCGTTGCCAGAATGCAGAGAAATTTA-TGTCCAGCACCACCA
C-DAF.seq       TGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAGCACCACCA
RC of B/C DAF   TGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAGCACCACCA
```

Fig. 9 (part 4 of 11)

```
                        760       770       780       790       800       810
                          |         |         |         |         |         |
5/P5          CAAATTGACA-TGGAATAATCCAGGGGAACGTTGACCATTATGGATATAAACG-----
C-DAF.seq     CAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATTATGGATATAGACAGTCTG
RC of B/C DAF CAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATTATGGATATAGACAGTCTG

                  820       830       840       850       860       870
                    |         |         |         |         |         |
5/P5          ----------------------------------------------------------
C-DAF.seq     TAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGCACTCTATTTATTGTAC
RC of B/C DAF TAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGCACTCTATTTATTGTAC

                    880       890       900       910       920
                      |         |         |         |         |
5/P5          ----------------------------------------------------------
C-DAF.seq     TGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAATGCAGAGGAAAATCT
RC of B/C DAF TGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAATGCAGAGGAAAATCT
```

Fig. 9 (part 5 of 11)

```
                    930       940       950       960       970       980
                      |         |         |         |         |         |
5/P5             -----------------------------------------------------------
C-DAF.seq        CTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAAATGTTCCAACTA
RC of B/C DAF    CTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAAATGTTCCAACTA

                     990      1000      1010      1020      1030      1040
                       |         |         |         |         |         |
5/P5             -----------------------------------------------------------
C-DAF.seq        CAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACACCAAATGCTCA
RC of B/C DAF    CAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACACCAAATGCTCA

                     1050      1060      1070      1080      1090      1100
                        |         |         |         |         |         |
5/P5             -----------------------------------------------------------
C-DAF.seq        AGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAACAACCCCA
RC of B/C DAF    AGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAACAACCCCA

                      1110      1120      1130      1140      1150      1160
                         |         |         |         |         |         |
5/P5             -----------------------------------------------------------
C-DAF.seq        AATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTT
RC of B/C DAF    AATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTT
```

Fig. 9 (part 6 of 11)

```
                     1170      1180      1190      1200      1210
                       |         |         |         |         |
5/P5            ----------------------------------------------------------
C-DAF.seq       TCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGCCAAA
RC of B/C DAF   TCAC

               1220      1230      1240      1250      1260      1270
                 |         |         |         |         |         |
5/P5            ----------------------------------------------------------
C-DAF.seq       GAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGACTT
RC of B/C DAF   ----------------------------------------------------------

                 1280      1290      1300      1310      1320      1330
                   |         |         |         |         |         |
5/P5            ----------------------------------------------------------
C-DAF.seq       ATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTG
RC of B/C DAF   ----------------------------------------------------------
```

Fig. 9 (part 7 of 11)

```
                  1340      1350      1360      1370      1380      1390
                     |         |         |         |         |         |
5/P5         ------------------------------------------------------------
C-DAF.seq    TCTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCAGTCCTGGAAT
RC of B/C DAF ------------------------------------------------------------

                  1400      1410      1420      1430      1440      1450
                     |         |         |         |         |         |
5/P5         ------------------------------------------------------------
C-DAF.seq    CACATTCTTAGCACACCTACACCTCTTGAAAATAGAACAACTTGCAGAATTGAGAGTG
RC of B/C DAF ------------------------------------------------------------

                  1460      1470      1480      1490      1500
                     |         |         |         |         |
5/P5         ------------------------------------------------------------
C-DAF.seq    ATTCCTTTCCTAAAAGTGTAAGAAAGCATAGAGATTTGTTCGTATTTAGAATGGGATC
RC of B/C DAF ------------------------------------------------------------
```

Fig. 9 (part 8 of 11)

```
            1510      1520      1530      1540      1550      1560
              |         |         |         |         |         |
5/P5         ----------------------------------------------------------
C-DAF.seq    ACGAGGAAAAGAGAAGGAAAGTGATTTTTTTCCACAAGATCTGTAATGTTATTTCCAC
RC of B/C DAF ----------------------------------------------------------

              1570      1580      1590      1600      1610      1620
                |         |         |         |         |         |
5/P5         ----------------------------------------------------------
C-DAF.seq    TTATAAAGGAAATAAAAAATGAAAAACATTATTTGGATATCAAAAGCAAATAAAAACC
RC of B/C DAF ----------------------------------------------------------

                1630      1640      1650      1660      1670      1680
                  |         |         |         |         |         |
5/P5         ----------------------------------------------------------
C-DAF.seq    CAATTCAGTCTCTTCTAAGCAAAATTGCTAAAGAGAGATGAACCACATTATAAAGTAA
RC of B/C DAF ----------------------------------------------------------

                  1690      1700      1710      1720      1730      1740
                    |         |         |         |         |         |
5/P5         ----------------------------------------------------------
C-DAF.seq    TCTTTGGCTGTAAGGCATTTTCATCTTTCCTTCGGGTTGGCAAAATATTTTAAAGGTA
RC of B/C DAF ----------------------------------------------------------
```

Fig. 9 (part 9 of 11)

18/23

```
             1750      1760      1770      1780      1790
                |         |         |         |         |
5/P5          ----------------------------------------------------------
C-DAF.seq     AAACATGCTGGTGAACCAGGGGTGTTGATGGTGATAAGGGAGGAATATAGAATGAAAG
RC of B/C DAF ----------------------------------------------------------

              1800      1810      1820      1830      1840      1350
                 |         |         |         |         |         |
5/P5          ----------------------------------------------------------
C-DAF.seq     ACTGAATCTTCCTTTGTTGCACAAATAGAGTTTGGAAAAAGCCTGTGAAAGGTGTCTT
RC of B/C DAF ----------------------------------------------------------

               1860      1870      1880      1890      1900      1910
                  |         |         |         |         |         |
5/P5          ----------------------------------------------------------
C-DAF.seq     CTTTGACTTAATGTCTTTAAAAGTATCCAGAGATACTACAATATTAACATAAGAAAAG
RC of B/C DAF ----------------------------------------------------------

                1920      1930      1940      1950      1960      1970
                   |         |         |         |         |
5/P5          ----------------------------------------------------------
C-DAF.seq     ATTATATATTATTTCTGAATCGAGATGTCCATAGTCAAATTTGTAAATCTTATTCTTT
RC of B/C DAF ----------------------------------------------------------
```

Fig. 9 (part 10 of 11)

```
                     1980      1990      2000      2010      2020      2030
                        |         |         |         |         |         |
5/P5          ----------------------------------------------------------
C-DAF.seq     TGTAATATTTATTTATATTTATTTATGACAGTGAACATTCTGATTTTACATGTAAAAC
RC of B/C DAF ----------------------------------------------------------

                      2040      2050      2060      2070      2080
                         |         |         |         |         |
5/P5          -----------------------------------------------------------
C-DAF.seq     AAGAAAAGTTGAAGAAGATATGTGAAGAAAAAATGTATTTTTCCTAAATAGAAATAAAT
RC of B/C DAF -----------------------------------------------------------

             2090      2100
                |         |
5/P5          ---------------T
C-DAF.seq     GATCCCATTTTTTGGT
RC of B/C DAF ----------------
```

Fig. 9 (part 11 of 11)

```
1                                                        CC GCT GGG CGT AGC

15    TGC GAC TCG GCG GAG TCC CGG CGG CGC GTC CTT GTT CTA ACC CGG CGC GCC
      |<-- Leader sequence
      Met Thr Val Ala Arg Pro Ser Val Pro Ala Ala Leu Pro Leu Leu Gly Glu  17
66    ATG ACC GTC GCG CGG CCG AGC GTG CCC GCG GCG CTG CCC CTC CTC GGG GAG

      Leu Pro Arg Leu Leu Leu Leu Val Leu Leu Cys Leu Pro Ala Val Trp Gly  34
117   CTG CCC CGG CTG CTG CTG CTG GTG CTG TTG TGC CTG CCG GCC GTG TGG GGT
       <- sushi 1
      |<-- mature sequence (first 16 amino acids sequenced)
      Asp Cys Gly Leu Pro Pro Asp Val Pro Asn Ala Gln Pro Ala Leu Glu Gly  51
168   GAC TGT GGC CTT CCC CCA GAT GTA CCT AAT GCC CAG CCA GCT TTG GAA GGC

      Arg Thr Ser Phe Pro Glu Asp Thr Val Ile Thr Tyr Lys Cys Glu Glu Ser  68
219   CGT ACA AGT TTT CCC GAG GAT ACT GTA ATA ACG TAC AAA TGT GAA GAA AGC

      Phe Val Lys Ile Pro Gly Glu Lys Asp Ser Val Ile Cys Leu Lys Gly Ser  85
270   TTT GTG AAA ATT CCT GGC GAG AAG GAC TCA GTG ATC TGC CTT AAG GGC AGT
                                    sushi 1 ->|    |sushi 2
      Gln Trp Ser Asp Ile Glu Glu Phe Cys Asn Arg Ser Cys Glu Val Pro Thr 102
321   CAA TGG TCA GAT ATT GAA GAG TTC TGC AAT CGT AGC TGC GAG GTG CCA ACA

      Arg Leu Asn Ser Ala Ser Leu Lys Gln Pro Tyr Ile Thr Gln Asn Tyr Phe 119
372   AGG CTA AAT TCT GCA TCC CTC AAA CAG CCT TAT ATC ACT CAG AAT TAT TTT

      Pro Val Gly Thr Val Val Glu Tyr Glu Cys Arg Pro Gly Tyr Arg Arg Glu 136
423   CCA GTC GGT ACT GTT GTG GAA TAT GAG TGC CGT CCA GGT TAC AGA AGA GAA

      Pro Ser Leu Ser Pro Lys Leu Thr Cys Leu Gln Asn Leu Lys Trp Ser Thr 153
474   CCT TCT CTA TCA CCA AAA CTA ACT TGC CTT CAG AAT TTA AAA TGG TCC ACA
                  sushi 2->|        |<- sushi 3
      Ala Val Glu Phe Cys Lys Lys Lys Ser Cys Pro Asn Pro Gly Glu Ile Arg 170
525   GCA GTC GAA TTT TGT AAA AAG AAA TCA TGC CCT AAT CCG GGA GAA ATA CGA

      Asn Gly Gln Ile Asp Val Pro Gly Gly Ile Leu Phe Gly Ala Thr Ile Ser 187
576   AAT GGT CAG ATT GAT GTA CCA GGT GGC ATA TTA TTT GGT GCA ACC ATC TCC

      Phe Ser Cys Asn Thr Gly Tyr Lys Leu Phe Gly Ser Thr Ser Ser Phe Cys 204
627   TTC TCA TGT AAC ACA GGG TAC AAA TTA TTT GGC TCG ACT TCT AGT TTT TGT
                                                           sushi 3 ->|
      Leu Ile Ser Gly Ser Ser Val Gln Trp Ser Asp Pro Leu Pro Glu Cys Arg 221
678   CTT ATT TCA GGC AGC TCT GTC CAG TGG AGT GAC CCG TTG CCA GAG TGC AGA
              |<- sushi 4
      Glu Ile Tyr Cys Pro Ala Pro Pro Gln Ile Asp Asn Gly Ile Ile Gln Gly 238
729   GAA ATT TAT TGT CCA GCA CCA CCA CAA ATT GAC AAT GGA ATA ATT CAA GGG
```

Fig. 10 (part 1 of 2)

```
     Glu Arg Asp His Tyr Gly Tyr Arg Gln Ser Val Thr Tyr Ala Cys Asn Lys 255
780  GAA CGT GAC CAT TAT GGA TAT AGA CAG TCT GTA ACG TAT GCA TGT AAT AAA

     Gly Phe Thr Met Ile Gly Glu His Ser Ile Tyr Cys Thr Val Asn Asn Asp 272
831  GGA TTC ACC ATG ATT GGA GAG CAC TCT ATT TAT TGT ACT GTG AAT AAT GAT
                                             sushi 4->|
     Glu Gly Glu Trp Ser Gly Pro Pro Pro Glu Cys Arg Gly Lys Ser Leu Thr 289
885  GAA GGA GAG TGG AGT GGC CCA CCA CCT GAA TGC AGA GGA AAA TCT CTA ACT

     Ser Lys Val Pro Pro Thr Val Gln Lys Pro Thr Thr Val Asn Val Pro Thr 306
933  TCC AAG GTC CCA CCA ACA GTT CAG AAA CCT ACC ACA GTA AAT GTT CCA ACT

     Thr Glu Val Ser Pro Thr Ser Gln Lys Thr Thr Thr Lys Thr Thr Thr Pro 323
984  ACA GAA GTC TCA CCA ACT TCT CAG AAA ACC ACC ACA AAA ACC ACC ACA CCA

     Asn Ala Gln Ala Thr Arg Ser Thr Pro Val Ser Arg Thr Thr Lys His Phe 340
1035 AAT GCT CAA GCA ACA CGG AGT ACA CCT GTT TCC AGG ACA ACC AAG CAT TTT

     His Glu Thr Thr Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly Thr Thr Arg 357
1086 CAT GAA ACA ACC CCA AAT AAA GGA AGT GGA ACC ACT TCA GGT ACT ACC CGT

     Leu Leu Ser Gly His Thr Cys Phe Thr Leu Thr Gly Leu Leu Gly Thr Leu 374
1137 CTT CTA TCT GGG CAC ACG TGT TTC ACG TTG ACA GGT TTG CTT GGG ACG CTA

     Val Thr Met Gly Leu Leu Thr Stop                                    381
1188 GTA ACC ATG GGC TTG CTG ACT TAG CCAAAGAAGAGTTAAGAAG

1231 AAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGACTTATCTGCATATTGGATAAAATAAA
1298 TGCAATTGTGCTCTTCATTTAGGATGCTTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACAGAGC
1365 AAGGAGAAAAAAGGCAGTCCTGGAATCACATTCTTAGCACACCTACACCTCTTGAAAATAGAACAAC
1432 TTGCAGAATTGAGAGTGATTCCTTTCCTAAAAGTGTAAGAAAGCATAGAGATTTGTTCGTATTTAGA
1499 ATGGGATCACGAGGAAAAGAGAAGGAAAGTGATTTTTTTCCACAAGATCTGTAATGTTATTTCCACT
1566 TATAAAGGAAATAAAAAATGAAAAACATTATTTGGATATCAAAAGCAAATAAAAACCCAATTCAGTC
1633 TCTTCTAAGCAAAATTGCTAAAGAGAGATGAACCACATTATAAAGTAATCTTTGGCTGTAAGGCATT
1700 TTCATCTTTCCTTCGGGTTGGCAAAATATTTTAAAGGTAAAACATGCTGGTGAACCAGGGGTGTTGA
1767 TGGTGATAAGGGAGGAATATAGAATGAAAGACTGAATCTTCCTTTGTTGCACAAATAGAGTTTGGAA
1834 AAAGCCTGTGAAAGGTGTCTTCTTTGACTTAATGTCTTTAAAAGTATCCAGAGATACTACAATATTA
1901 ACATAAGAAAAGATTATATATTATTTCTGAATCGAGATGTCCATAGTCAAATTTGTAAATCTTATTC
1968 TTTTGTAATATTTATTTATATTTATTTATGACAGTGAACATTCTGATTTTACATGTAAAACAAGAAA
2035 AGTTGAAGAAGATATGTGAAGAAAAATGTATTTTTCCTAAATAGAAATAAATGATCCCATTTTTTGG
2102 T
```

Fig. 10 (part 2 of 2)

```
  1    TTTAAACGGGCCCTCTAGACTCGAGCGGCCGCTGCCCATCTTGTCGTCGTCGTCCTTGTAGTCG
 65  TGCATGTGGTGGTGGTGGTGGTGGTTAACCATGGTGGCGGGCCGCCACTGTGCTGGATATCTGCAGA
132  ATTCGATGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCC

     Met Thr Val Ala Arg Pro Ser Val Pro Ala Ala Leu Pro Leu Leu Gly Glu  17
199  ATG ACC GTC GCG CGG CCG AGC GTG CCC GCG GCG CTG CCC CTC CTC GGG GAG

     Leu Pro Arg Leu Leu Leu Leu Val Leu Leu Cys Leu Pro Ala Val Trp Gly  34
250  CTG CCC CGG CTG CTG CTG CTG GTG CTG TTG TGC CTG CCG GCC GTG TGG GGT

     Asp Cys Gly Leu Pro Pro Asp Val Pro Asn Ala Gln Pro Ala Leu Glu Gly  51
301  GAC TGT GGC CTT CCC CCA GAT GTA CCT AAT GCC CAG CCA GCT TTG GAA GGC

     Arg Thr Ser Phe Pro Glu Asp Thr Val Ile Thr Tyr Lys Cys Glu Glu Ser  68
352  CGT ACA AGT TTT CCC GAG GAT ACT GTA ATA ACG TAC AAA TGT GAA GAA AGC

     Phe Val Lys Ile Pro Gly Glu Lys Asp Ser Val Ile Cys Leu Lys Gly Ser  85
403  TTT GTG AAA ATT CCT GGC GAG AAG GAC TCA GTG ATC TGC CTT AAG GGC AGT

     Gln Trp Ser Asp Ile Glu Glu Phe Cys Asn Arg Ser Cys Glu Val Pro Thr 102
454  CAA TGG TCA GAT ATT GAA GAG TTC TGC AAT CGT AGC TGC GAG GTG CCA ACA

     Arg Leu Asn Ser Ala Ser Leu Lys Gln Pro Tyr Ile Thr Gln Asn Tyr Phe 119
505  AGG CTA AAT TCT GCA TCC CTC AAA CAG CCT TAT ATC ACT CAG AAT TAT TTT

     Pro Val Gly Thr Val Val Glu Tyr Glu Cys Arg Pro Gly Tyr Arg Arg Glu 136
556  CCA GTC GGT ACT GTT GTG GAA TAT GAG TGC CGT CCA GGT TAC AGA AGA GAA

     Pro Ser Leu Ser Pro Lys Leu Thr Cys Leu Gln Asn Leu Lys Trp Ser Thr 153
607  CCT TCT CTA TCA CCA AAA CTA ACT TGC CTT CAG AAT TTA AAA TGG TCC ACA

     Ala Val Glu Phe Cys Lys Lys Lys Ser Cys Pro Asn Pro Gly Glu Ile Arg 170
658  GCA GTC GAA TTT TGT AAA AAG AAA TCA TGC CCT AAT CCG GGA GAA ATA CGA

     Asn Gly Gln Ile Asp Val Pro Gly Gly Ile Leu Phe Gly Ala Thr Ile Ser 187
709  AAT GGT CAG ATT GAT GTA CCA GGT GGC ATA TTA TTT GGT GCA ACC ATC TCC

     Phe Ser Cys Asn Thr Gly Tyr Lys Leu Phe Gly Ser Thr Ser Ser Phe Cys 204
760  TTC TCA TGT AAC ACA GGG TAC AAA TTA TTT GGC TCG ACT TCT AGT TTT TGT
```

Fig. 11 (part 1 of 2)

```
     Leu Ile Ser Gly Ser Ser Val Gln Trp Ser Asp Pro Leu Pro Glu Cys Arg 221
811  CTT ATT TCA GGC AGC TCT GTC CAG TGG AGT GAC CCG TTG CCA GAG TGC AGA

     Glu Ile Tyr Cys Pro Ala Pro Pro Gln Ile Asp Asn Gly Ile Ile Gln Gly 238
862  GAA ATT TAT TGT CCA GCA CCA CCA CAA ATT GAC AAT GGA ATA ATT CAA GGG

     Glu Arg Asp His Tyr Gly Tyr Arg Gln Ser Val Thr Tyr Ala Cys Asn Lys 255
913  GAA CGT GAC CAT TAT GGA TAT AGA CAG TCT GTA ACG TAT GCA TGT AAT AAA

     Gly Phe Thr Met Ile Gly Glu His Ser Ile Tyr Cys Thr Val Asn Asn Asp 272
964  GGA TTC ACC ATG ATT GGA GAG CAC TCT ATT TAT TGT ACT GTG AAT AAT GAT

     Glu Gly Glu Trp Ser Gly Pro Pro Pro Glu Cys Arg Gly Lys Ser Leu Thr 289
1015 GAA GGA GAG TGG AGT GGC CCA CCA CCT GAA TGC AGA GGA AAA TCT CTA ACT

     Ser Lys Val Pro Pro Thr Val Gln Lys Pro Thr Thr Val Asn Val Pro Thr 306
1066 TCC AAG GTC CCA CCA ACA GTT CAG AAA CCT ACC ACA GTA AAT GTT CCA ACT

     Thr Glu Val Ser Pro Thr Ser Gln Lys Thr Thr Thr Lys Thr Thr Thr Pro 323
1117 ACA GAA GTC TCA CCA ACT TCT CAG AAA ACC ACC ACA AAA ACC ACC ACA CCA

     Asn Ala Gln Ala Thr Arg Ser Thr Pro Val Ser Arg Thr Thr Lys His Phe 340
1168 AAT GCT CAA GCA ACA CGG AGT ACA CCT GTT TCC AGG ACA ACC AAG CAT TTT

     His Glu Thr Thr Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly Thr Thr Arg 357
1219 CAT GAA ACA ACC CCA AAT AAA GGA AGT GGA ACC ACT TCA GGT ACT ACC CGT

     Leu Leu Ser Gly His Thr Cys Phe Thr Leu Thr Gly Leu Leu Gly Thr Leu 374
1270 CTT CTA TCT GGG CAC ACG TGT TTC ACG TTG ACA GGT TTG CTT GGG ACG CTA

     Val Thr Met Gly Leu Leu Thr Stop                                    381
1321 GTA ACC ATG GGC TTG CTG ACT TAG CCAAAGAAGAGTTAAGAAGAAAATACACACAAGTA

1380 TACAGACTGTTCCTAGTTTCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTC
1447 ATTTAGGATGCTTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACA
```

Fig. 11 (part 2 of 2)